

## Anticipating future genetic needs for French dairy and suckler cattle sectors.

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Session 58 Theatre 3

Anticipating future genetic needs for French dairy and suckler cattle sectors H. Lagarde<sup>1</sup>, P. Martin<sup>1</sup>, D. Boichard<sup>1</sup>

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The French dairy and suckler cattle sectors are expected to face major challenges over the next 20 years, such as a probable decline in beef consumption, an increase of heat waves, the emergence of new pathogens, constraints on environmental impact, the sensitivity of forage crops to drought, a shrinking number of farmers or volatile input costs. These changes are likely to lead to significant transformation of livestock production systems. Thus, current bovine genetic resources may not be suitable for these future systems and therefore need to be reinvestigated. Altering genetic resources being a long-term process, it is essential to think now about the objectives of cattle breeding programmes in order to meet future genetic resources needs. To this end, an interdisciplinary group of cattle experts from various fields (macroeconomics, production systems, ecology, feed production, nutrition, physiology, veterinary sciences, genetics, human and social sciences, public policies) has been set up to define scenarios for the evolution of cattle farming systems in France 20 years ahead, as well as the genetic resources fitting these changes. The expert group identified factors with the greatest potential impact on future cattle farming systems, constructed several plausible cattle farming system evolution scenarios based on the trends of these factors and determined the suitable genetic resources fitting them. Results obtained were then presented and discussed with shareholders of the bovine sector to obtain feedback on the relevance, acceptability and feasibility of these findings. This work was supported by a French government grant managed by the Agence Nationale de Recherche under the France2030 program "ANR-22-PEAE-0003".

Session 58 Theatre 4

Investigating genomic adaptation to climate in local Mediterranean sheep breeds

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Since domestication, livestock followed human migrations, generating several locally adapted breeds. Hence, autochthonous populations often present adaptive traits unobserved in cosmopolitan highly-productive breeds. Using a landscape genomics approach, we investigated genetic signatures of environmental adaptation in 1291 individuals belonging to 63 Mediterranean sheep breeds, genotyped using the Illumina OvineSNP50 beadchip. We used Sam ada v0.8.3 to identify genotype/environment associations with 13 environmental variables and correcting for the ancestry fractions identified through ADMIXTURE. Finally, we recorded the genes intercepted by neighboring regions in linkage disequilibrium with each significantly associated SNP. We identified candidate genes of which many have known roles in environmental adaptation. Noticeably, by applying candidate gene prioritization we identified genes putatively involved in metabolic pathways that are particularly relevant, as response to the ever-changing climate conditions (e.g. increasing temperatures and UV-radiations).